

Bartam

#8

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/507,928
Source: PCP/10
Date Processed by STIC: 6/10/05

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 06/10/2005
PATENT APPLICATION: US/10/507,928 TIME: 10:08:51

Input Set : A:\Sequence Listing
Output Set: N:\CRF4\06102005\J507928.raw

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3 <110> APPLICANT: POWDERMED LIMITED AND GLAXO GROUP LIMITED
5 <120> TITLE OF INVENTION: ADJUVANT
7 <130> FILE REFERENCE: N.88232B GCW
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/507,928
C--> 9 <141> CURRENT FILING DATE: 2004-09-17
9 <160> NUMBER OF SEQ ID NOS: 12
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 12
15 <212> TYPE: PRT
16 <213> ORGANISM: Artificial sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: HBsAg in BLAB/C mice
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27 <210> SEQ ID NO: 2
28 <211> LENGTH: 9
29 <212> TYPE: PRT
30 <213> ORGANISM: Artificial sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: HSV CD8 in BLAB/C mice
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42 <211> LENGTH: 1503
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: nucleotide sequence of p55 gag insert in pGagOptprpr2
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54 cttgaacgggt ttgcgtgaa cccaggcctg ctggaaacat ctgagggatg tcggccagatc 180
56 ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac 240
58 acagtggcta ccctctactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc 300
60 ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggcccagca ggcagctgct 360
62 gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcaggc 420
64 cagatggttc atcaggccat cagccccccc acgctcaatg cctgggtgaa ggttgtcga 480
66 gagaaggcct tttctcctga ggttatcccc atgttctccg ctttgagtgaa gggggccact 540
68 cctcaggacc tcaataataat gcttaataacc gtggggcggcc atcaggccgc catgcaaatg 600
70 ttgaaggaga ctatcaacga ggaggcagcc gagtgggaca gagtgcattc cgccacgct 660

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74	tctacactgc	aagagcaa	at	cgatggatg	accaacaatc	ctcccatccc	agttggagaa	780								
76	atctataaac	ggtggatcat	tctcggtctc	aataaaattg	ttagaatgta	ctctccgaca	840									
78	tccatccttgc	acattagaca	gggacccaaa	gagccttta	gggattacgt	cgaccggtt	900									
80	tataagaccc	tgcgagcaga	gcaggcctct	caggaggtca	aaaactggat	gacggagaca	960									
82	ctcctggta	agaacgctaa	ccccgactgc	aaaacaatct	tgaaggcact	aggccggct	1020									
84	gccaccctgg	aagagatgat	gaccgcctgt	cagggagtag	gcccggcc	acacaaagcc	1080									
86	agagtgttgg	ccgaagccat	gagccaggtg	acgaactccg	caaccatcat	gatcagaga	1140									
88	gggaacttcc	gcaatcagcg	gaagatcg	aagtgttca	attgcggcaa	ggagggtcat	1200									
90	accgcccgc	actgtcggc	ccctaggaag	aaagggtgtt	ggaagtgcgg	caaggaggga	1260									
92	caccagatga	aagactgtac	agaacgacag	gccaatttc	ttggaaagat	ttggccgagc	1320									
94	tacaagggga	gacctgtta	tttcctgcaa	agcaggccc	agccaccgc	ccccctgag	1380									
96	gaatccttca	ggtccggagt	ggagaccaca	acgcctcccc	aaaaacagga	accaatcgac	1440									
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118							20			25						30
121	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
122							35			40						45
125	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
126							50			55						60
129	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
130	65						70			75						80
133	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
134							85			90						95
137	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
138							100			105						110
141	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
142							115			120						125
145	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
146							130			135						140
149	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
150	145						145			150						160
153	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
154							165			170						175
157	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
158							180			185						190
161	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
162							195			200						205
165	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala

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166	210	215	220
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170	225	230	235
173	Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile		240
174	245	250	255
177	Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys		
178	260	265	270
181	Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly		
182	275	280	285
185	Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu		
186	290	295	300
189	Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr		
190	305	310	315
193	Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala		320
194	325	330	335
197	Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly		
198	340	345	350
201	Val Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser		
202	355	360	365
205	Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg		
206	370	375	380
209	Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His		
210	385	390	395
213	Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys		
214	405	410	415
217	Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn		
218	420	425	430
221	Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe		
222	435	440	445
225	Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg		
226	450	455	460
229	Ser Gly Val Glu Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp		
230	465	470	475
233	Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp		480
234	485	490	495
237	Pro Ser Ser Gln		
238	500		
241	<210> SEQ ID NO: 5		
242	<211> LENGTH: 1515		
243	<212> TYPE: DNA		
244	<213> ORGANISM: Artificial sequence		
246	<220> FEATURE:		
247	<223> OTHER INFORMATION: nucleotide sequence of the p17/24trNEF insert in p17/24trNEF1		
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252	ttaaggccag gggaaagaa aaaataaaa taaaaacata tagtatggc aagcagggag	120	
254	ctagaacgat tcgcagttaa tcctggctg ttagaaacat cagaagctg tagacaataa	180	
256	ctgggacagc tacaaccatc cttcagaca ggatcagaag aacttagatc attatataat	240	
258	acagtagcaa ccctctattt tgtgcatcaa aggatagaga taaaagacac caaggaagct	300	

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260	ttagacaaga	tagaggaaga	gcaaaacaaa	agtaagaaaa	aagcacagca	agcagcagct	360
262	gacacaggac	acagacaatca	ggtcagccaa	aattacccta	tagtgcagaa	catccagggg	420
264	caaatggta	cacggccat	atcacctaga	actttaaatg	catggtaaa	agttagtagaa	480
266	gagaaggctt	tcagcccaga	agtatacc	atgtttcag	cattatcaga	aggagccacc	540
268	ccacaagatt	taaacaccat	gctaaacaca	gtggggggac	atcaagcagc	catgcaaatg	600
270	ttaaaagaga	ccatcaatga	ggaagctgca	aatgggata	gagtgcattc	agtgcattgca	660
272	gggcctattg	caccaggcca	gatgagagaa	ccaagggaa	gtgacatagc	aggaactact	720
274	agtacccttc	aggaacaaat	aggatggat	acaaataatc	cacctatccc	agtaggagaa	780
276	atttataaaa	gatggataat	cctgggatta	aataaaatag	taagaatgt	tagccctacc	840
278	agcattctgg	acataagaca	aggaccaaaa	gaaccctta	gagactatgt	agaccggttc	900
280	tataaaactc	taagagccga	gcaagcttca	caggaggtaa	aaaattggat	gacagaaacc	960
282	ttgttggtcc	aaaatgcgaa	cccagattgt	aagactattt	taaaagcatt	gggaccagcg	1020
284	gctacactag	aagaaatgtat	gacagcatgt	cagggagtag	gaggaccgg	ccataaggca	1080
286	agagttttgg	tgggtttcc	agtcacacct	caggtacctt	taagaccaat	gacttacaag	1140
288	gcagctgtag	atcttagcca	cttttaaaa	gaaaaggggg	gactggaagg	gctaattcac	1200
290	tcccaaagaa	gacaagatat	ccttgatctg	tggatctacc	acacacaagg	ctactccct	1260
292	gattggcaga	actacacacc	agggccaggg	gtcagatatc	cactgacctt	tggatggtgc	1320
294	tacaagctag	taccagttga	gccagataag	gtagaagagg	ccaataaaagg	agagaacacc	1380
296	agcttggtag	accctgttag	cctgcatggg	atggatgacc	cggagagaga	agtgttagag	1440
298	tggaggttg	acagccacct	agcatttcat	cacgtggccc	gagagctgca	tccggagtac	1500
300	ttcaagaact	gctga					1515

303 <210> SEQ ID NO: 6

304 <211> LENGTH: 504

305 <212> TYPE: PRT

306 <213> ORGANISM: Artificial sequence

308 <220> FEATURE:

309 <223> OTHER INFORMATION: amino acid sequence of the p17/24trNEF insert in p17/24trNEF1

311 <400> SEQUENCE: 6

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318					20				25				30			
321	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
322					35				40			45				
325	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
326					50				55			60				
329	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
330	65				70				75			80				
333	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
334					85				90			95				
337	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
338					100				105			110				
341	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
342					115				120			125				
345	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
346					130				135			140				
349	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
350	145				150				155			160				
353	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser

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358	180	185	190
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362	195	200	205
365	Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala		
366	210	215	220
369	Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr		
370	225	230	235
373	Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile		
374	245	250	255
377	Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys		
378	260	265	270
381	Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly		
382	275	280	285
385	Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu		
386	290	295	300
389	Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr		
390	305	310	315
393	Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala		
394	325	330	335
397	Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly		
398	340	345	350
401	Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Val Gly Phe Pro Val		
402	355	360	365
405	Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp		
406	370	375	380
409	Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His		
410	385	390	395
413	400		
414	Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln		
417	405	410	415
418	Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg		
421	420	425	430
422	Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro		
425	435	440	445
426	Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His		
429	450	455	460
430	Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu		
433	465	470	475
434	Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu Leu		
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441	500		
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443	<211> LENGTH: 1518		
444	<212> TYPE: DNA		
445	<213> ORGANISM: Artificial sequence		
446	<220> FEATURE:		
447	<223> OTHER INFORMATION: nucleotide sequence of the p17/24opt/trNef insert in p17/24opt/tr		

VERIFICATION SUMMARY

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date